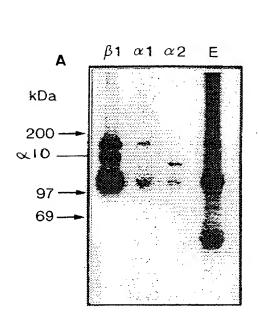
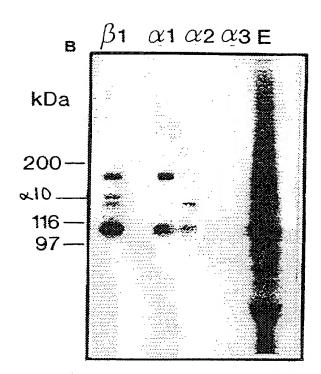


FIGURE 1

Peptide	Amino acid sequence
1	DNTAQTSAYIQYEPHHSI
2	GPGHWDR
3	AAFDGSGQR
4	FAMGALPD
5	FTASLDEWTTAAR
6	VDASFRPQGXLAP

3/22





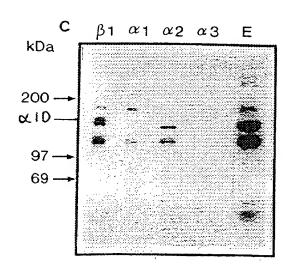


FIGURE 3

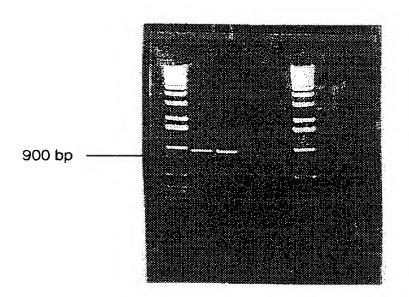


FIGURE 4

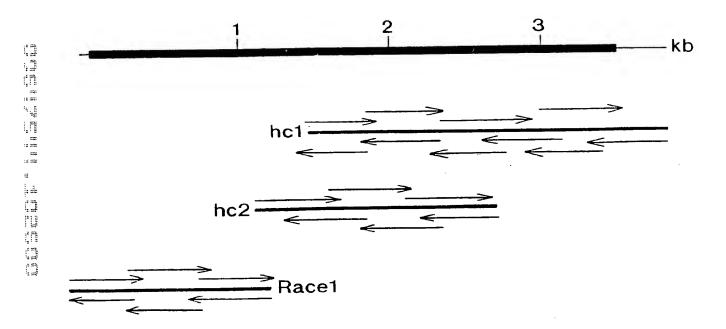


FIGURE 5

caggicagaaaccgatcaggcatggaactccccttcgtcactcac	72 -6	CATCUTGCCCAGAGGATTGCTGCTCCCTCATGCCACCATGCCTCAGCTACTTTTGGCCGAAGGTGTGGATGGT H P A Q R 1 $\lambda$ A $\lambda$ S M P H A L S Y P G R 3 V D G	1872 595
GOTTETCTCCCCCTTTTACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAGCTGAATTT G L C S P $_{\parallel}$ F N L D E H H P R L F P $_{\parallel}$ P $_{\parallel}$ P E A E F	144 19	COSCTAGATCTGGATGGAGATCATCTGGTCGATGTGGCTGCCCAGGGGGCAGCCATCCTGCTCAGC R L D L D G D D L V D V A V G A Q G A A I L L S	1944 619
GGATACAGTGTCTTACAACATGTTGGGGTGGACAGCGATGGATG	216 43	THE COCCUMENTATION CONTINUES AND THE POST OF THE POST	2016 643
TCAGGCGACCGGACGGGGACGTTTATCGCTCCCTGTAGGGGGGCCCCACAATCCCCCATGTGCCAAGGGC S G D R R G D V Y R C P V G G A H N A P C A K G	288	TGTAGGGGGGGGAGGCAGGAGGGAGTCTGTCTGCAGGGCCCTTTGCTTCCAAGTGACCTCCCGTACTCCC C R R R G Q E A V C L T A A L C P Q V T S R T P	2088 667
CACTTAGGTGACTACCACTGGGAAATTCATCTCATCCTGCTGGGAATATGCACCTGGGGATGTCTCTGTTA H L G D Y Q L G N S S N P A V N N N L G N S L L	360 91	GGTCGCTGGGTCACCAATTCTACATGAGGTTCACCGCATCACTGGATGAATGGACTGCTGGGGCACGTGCA	2106 691
GAGACAGATGGTGATGGGGGATTCATGGCCTGTGCCCCTCTCTGGTCTCTGTCTTGTGCAGCTGTGTCTTC E T D G D G G F H A C A P L W S R A C G S S V F	432 115	GCATTIGATGGCTCTGGCCAGAGGTTCTCCCCTCGGAGGCTCCGCCTCAGTGTGGGGAATGTCACTTGTGAG	2232 715
AGTICIGGGATATGTGCCCGTGTGGATGCTTCATTCCAGCCTCAGGGAAGCCTGGCACCCCATGCCCAACGC  S S G I C A R V D A S F O P O G S L A P T A Q R	504 139	CAGCTACACTTCCATGTGCTGGATACATCAGATTACCTCCGGCCAGTGGCCTTGACCTTTGCCTTG Q L H F H V L D T S D Y L R P V A L T V T F A L	2304 739
TOCCCAACATACATGGATGTTGTCATTGTCTTGGATGGCTCCAACAGCATCTACCCCTGGTCTGAAGTTCAGCCP T Y N N D V V I V L D G S N S I Y P W S E V Q	576 163	GACAMTACTACAAAGCCAGGCCTGTGCTGAATGAGGGCTCACCCACC	2376 763
ACCTTCCTACGAGACTGGTAGGGAAACTGTTTATTGACCCAGAACAGATACAGGTGGGACTGGTACAGTAT T F L R R L V G K L F I D P E Q I Q V G L V Q Y	648 187	TCANAGGATTCTGGCCCTGACAATGAATGTGTCACAGACCTGGTGCTTCAAGTGAATATGAGACATCAGAGGC S K D C G P D N E C V T D L V L Q V N M D I R G	2448 787
GGGGGGGCCCTGTACATGAGTGGTCCCTGGGAGGATTTCCGGACGAAGAAGAGAGTGGTGAGGAGCACCAAAG G E S P V H E W S L G D F R T K E E V V R A A K	720 211	TCCAGGAAGCCCCCATTTGTGGTTCGAGGTGGCCGGCGAAAGTGCTGGTATCTACAACTCTGGAGAAAGA S R K A P F V V R G G R R K V L V 5 T T L E N R	2520 #11
AACCTCAGTCGGCGGAGGACGAGAAACCAAAGACTGCCCAAGCAATAATGGTGGCCTGCACAGAAGGGTTC N L S R R E G R E T K T A Q A I M V A C T E G F	792 235	MAGANAATGETTACAATAEGAGEETGAGTATEATETTETETAGAAACCTECACCTGGCCAGTETCACTECT K E N A Y H T S L S I I F S R N L II L A S L T P	2592 835
AGTEAGTECEATGGGGGCCGACCCGAGGETGCCAGGCTACTGGTGGTGTCACTGATGGAGAGTCCCATGAT  S Q S H G G R P E A A R L L V V V T D G E S H D	864 259	CAGAGAGAGCCCAATANAGGTGGAATGTGCCGCCCCTTCTGCTCATGCCCGGCTCTGCAGTGTGGGGCAT Q R E S P I K V E C A A P S A H A R L C S V G H	2664 859
GGACAGGAGCTTCCTGCAGCACTAAAGGCCTGTGAGGCTGGAAGAGTGACACGCTATGGGATTGCAGTCCTT G E E L P A A L K A C E A G R V T R Y G I A V L	936 283	COTSTST TO CAGACT SEGMENT CAGACT THE CONTROL OF THE CONTROL C	2736 883
GUTCACTACCTCCGGCGCACCGACATCCCACCTCTTTCCTGAGAAAATTAGAACTATTGCAGTGATCA	1008 307	CAGGICTTIGGGAGCTGACIGCCAGCAGTGACAGCCTGGAGAAATGGCACCCTTCAAGAAAACACACCCQVFGGKLLTA SSDSLER NGTLQENTA	2808 901
DERFFFNVIDEAACTGAGGCTGCTCTGACTGACATTGTGGATGACTGAGGAGATCGG	1080 331	CMARCTEMECTMEATERNATATGACCCCCACCTCTTTTCTCTAGTGAGTCTACCCTGCACCCCTATGAG	2880 931
ATTITIGECTIGALEGECICATECACAMACCAMACCATECTTIGECTGCAMATGCTTACATTGGTTC	1152 355	GTICACCCATATGGGACCCTCCCAGTGGGCCCAGGATTCAAAACCACTCTCAGGGTTCAGAACCTA V H P Y G T L P V G P G P E F K T T L R V Q N L	2952 955
TCCACTCATCCCCTAAAGGATGGGATTCTTTTTGGGATGGTGGGGCCTATGACTGGGCAGGCTCTGTGCTA S T H R L K D G I L F G M V G A Y D W G G S V L	1224 379	GCCTGCTATGGGGCCATGGCCCTCATCACCTCCACCTGGGCCCATGGGGCCATGGGGCCATTACTTC G C Y V V S G L 1 I S $\lambda$ L L $\mu$ $\lambda$ V $\lambda$ H $\mu$ G $\mu$ Y $\mu$	3024 979
TOGETTGAAGGAGGCCACCCCTTTTCCCCCCACGAATGGCACTGGAAGACGAGTTCCCCCCTGCACTGCAG W L & G G H R L F P P R H A L & D & F P P A L Q	1296 403	CTATCACTGTCTCAAGTCATCACTAACAATGCAAGCTGCATAGTCCAAGACCCGAGGCCCA L S L S Q V I T N H A S C I V Q $\frac{N}{4}$ L T E P P G P	3096 1003
AACCATGCAGCCTACCTGGGTTACTCTGTTTCTTCCATCCTTTTGCGGGGTGGACCCCGCCTGTTTCTCTCT  H H A A Y L G Y S V S S H L L R G G R R L Y L S	1368 427	CCTGTGCATGCAGAGGAGCTTCAACACACAAACAGACTGAATGGGAGGAGAATACTCAGTGTGAGGGP V H P E E L Q H T N R L N G S N T Q C Q V V R	3168 1027
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	1440 451	TOCCALCITICOCCACCOCCAAACCGCACTCACGTCTCTGTTGGACTATTGAGGCTGGTTCACAATGAATTT C H L G Q L A K G T E V S V. G L L R L V H N E F	3240 1051
CCCCAGAGCCTCCAGGGGGAGCAGATTGGTTCATACTTTGGCAGTGAGCTCTGCCCATTGGATACAGATAGG A 0 3 L 0 G E 0 1 G S Y F G S E L C P L D T D R	1512 475	TTCCGAAGACCAAGTTCAAGTCCCTGACGGTGGTCAGCACCTTTGAGCTGGGAACCGAAGAGGGCAGTGTC F R R A K F K S L T V V S T F & L G T & & G S V	3312 1075
GATGGAACAACTGATGTCTTACTTGTGGCTGCCCCCATGTTCCTGGGACCCCAGAACAACGAACAACGAACACGT D G T T D V L L V A A P H F L G P Q N K B T G R	1584 199	CTACAGETGACGAGCCCCCCGTTGGAGTGAGCCCTCTTGGAGTGGTTCAGACCCGGCCTATCCTCATC L 0 L T E $\lambda$ 5 R M S E S L L E V V Q T R P 1 L $\underline{I}$	3384 1099
GTTTATGTGTATCTGGTAGGCCAGCAGTCCTTGGTGACCCTCCAAGGACACTTCAGCCAGAACCCCCCAG V Y V Y L V G Q Q S L L T L Q G T L Q P E P P Q	1656 523	TCCCTGTGGATCCTCATAGGCAGTGTCCTGGGAGGGTTGCTCTGCTTGCT	3456 1123
GATGCTCGGTTTGCCTTTGCCATGGGAGCTCTTCCTGATCTGAACCAAGATGGTTTTGCTGATGTGGCTGTG D A R F G F A M G A L P D L N Q D G F A D V A V	1728 547	AGCTTGGCTTCTTTGCCCATAGAMATCCCTGAGGAGAAAAAAAAGAAGAAGTTGGAGCAATGAATG	3528 1145
GGGGGCGCTCTGGALGATGGGCACCAGGGGGCCCTGTACCATGGALCCACAGTGGAGTCAGGCCC G A P L E D G H O G A L Y L Y H G T O S G V R P	1800 571	TAGANTAAGGETCTAGANAGTCCTCCCTGGCAGCTTTCTTCAAGAGACTTGCATANAAGCAGAGTTTGGGG GCTCAGATGGGCAAGAAGCCGCCTCTGGACTATCTCCCCAGACCAGCAGCCTGACTTGACTTTTGAGTCCT AGGATGCTGCTGCTAGAGATGAGCATTTACCTCAGACAAGAAGAGCTGGCAACAAAATAGCCATGCCTC CAACCTCTGCTTCCTCCTCCTGGTGATCCTGGTTCCATAGCCAACACTGGGGCTTTTTTTT	3672 3744

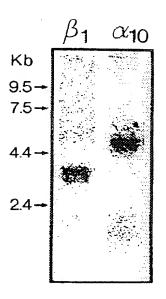
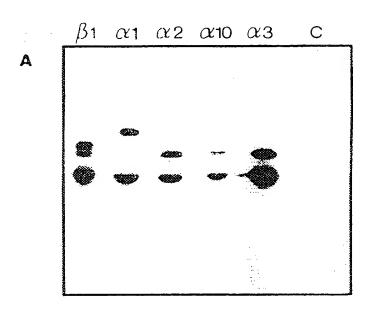


FIGURE 7



B IP: α10 β1 Blot: β1 β1

> 200 -97 -46 -

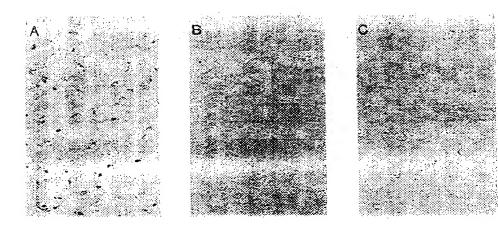
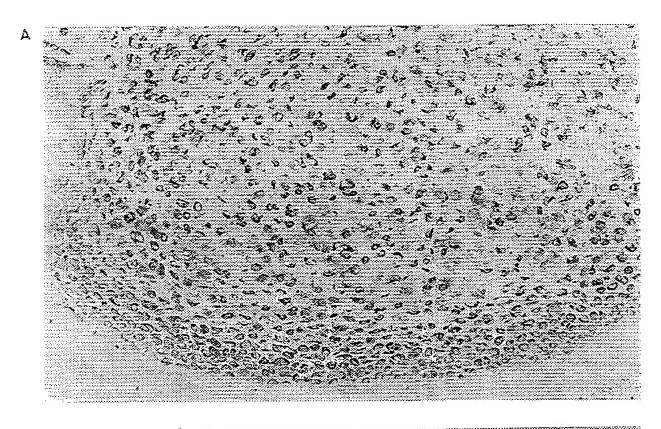


FIGURE 9



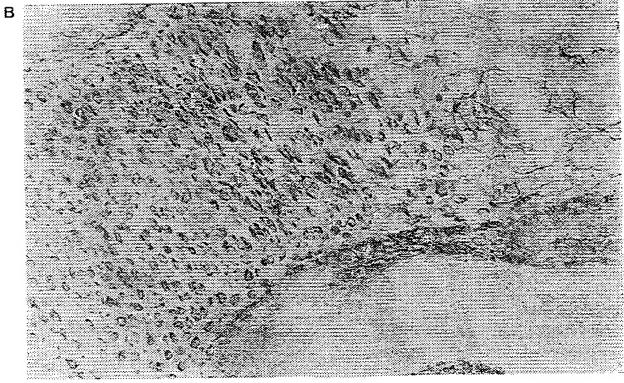
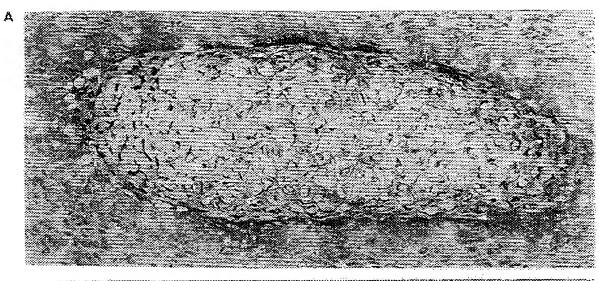
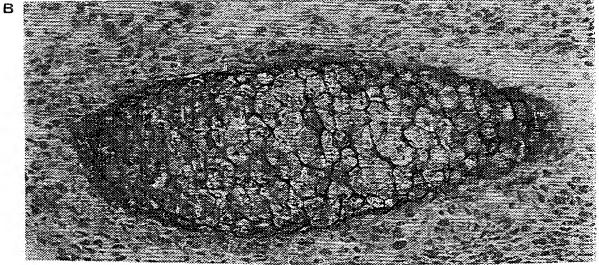


FIGURE 10





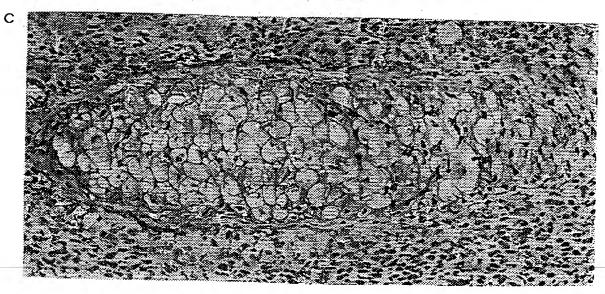
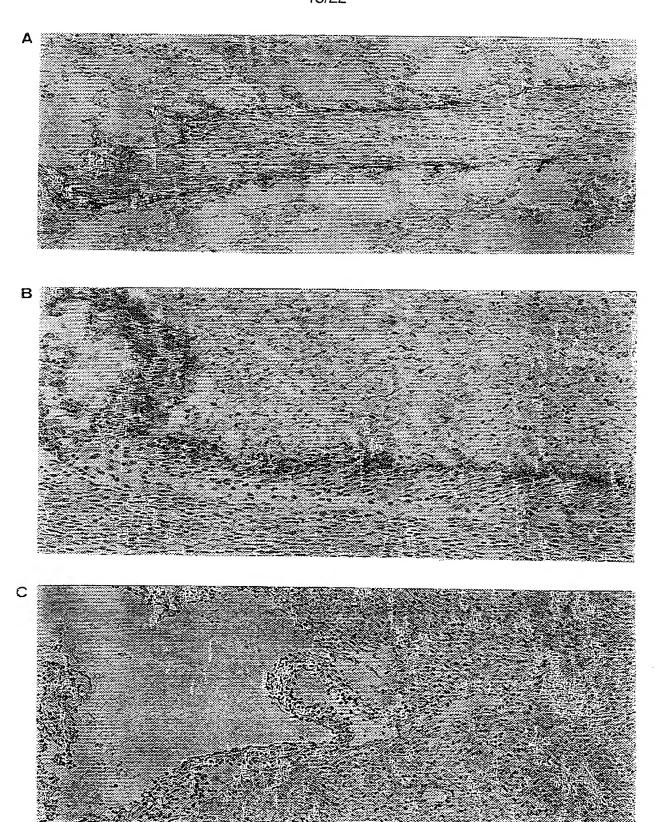
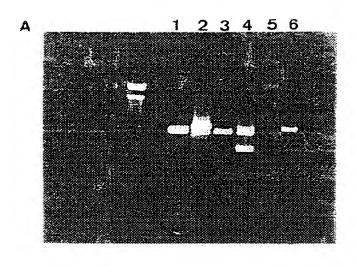


FIGURE 11

# Human RNA Master blot

Tissue	all expression	Tissue	$\alpha 10$ expression
Aorta	++++	Thyroid gland	-
Trachea	÷	Salivary gland	-
Lung	++	Spleen	•
Fetal lung	<del>++</del>	Fetal spleen	•
Kidney	<del>; 1</del>	Thymus	•
Fetal kidney	(+)	Fetal thymus	•
Heart	(÷)	Peripherial leucocyte	-
Fetal heart	++	Lymph node	-
Spinal cord	++	Appendix	-
Mammary gland	(+)	Placenta	-
Bone marrow	(+)	Whole brain	-
Small intestine	(+)	Fetal brain	-
Skeletal muscle	•	Amygdala	-
Liver	-	Caudate nucleus	-
Fetal liver	-	Cerebellum	-
Colon	•	Cerebral cortex	-
Bladder	-	Frontal lobe	-
Uterus	-	Hippocampus	•
Prostate	-	Medulla oblongata	•
Stomach	-	Occipitial lobe	•
Testis	-	Putamen	-
Ovary	•	Substantia nigra	-
Pancreas	-	Temporal lobe	-
Piutiatary gland	-	Thalamus	-
Adrenal gland	-	Subthalamic nucleus	-
	-		
		•	ETCI IDE 10





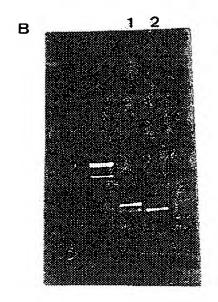
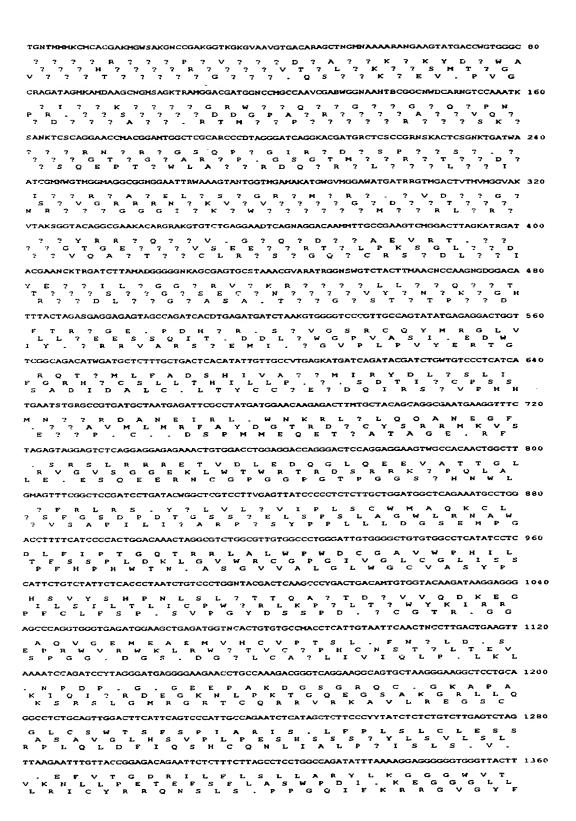
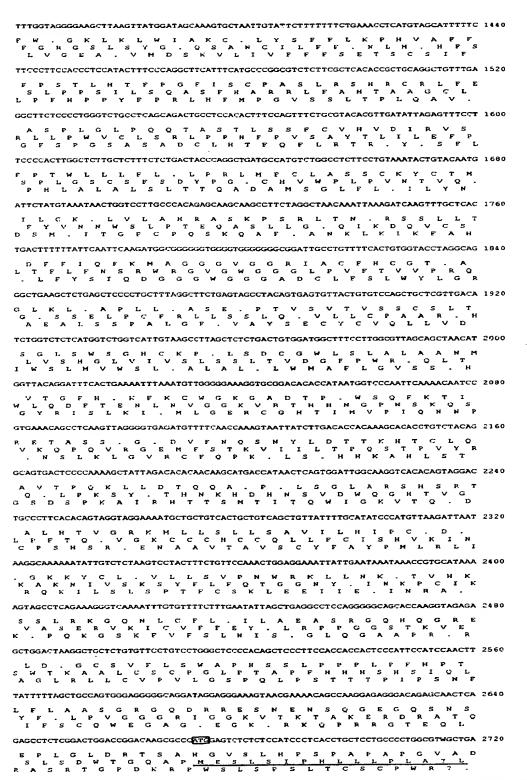


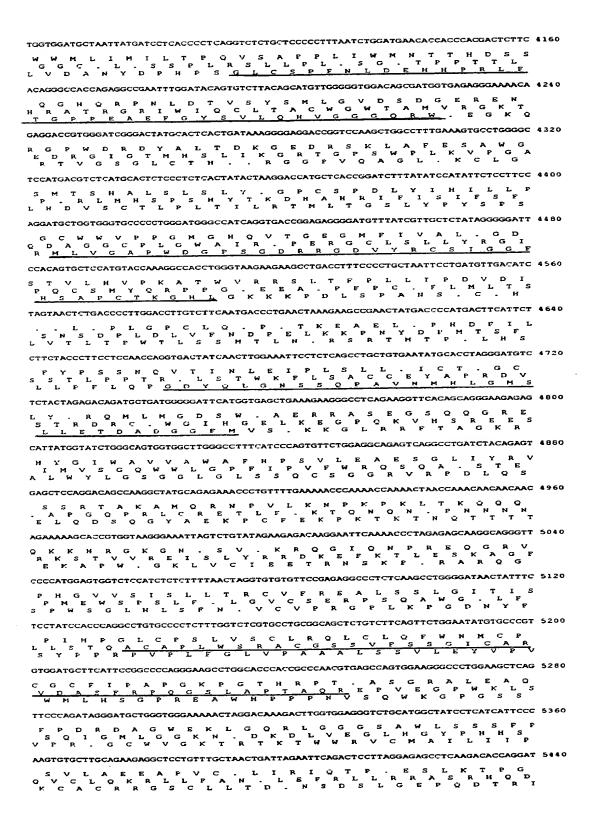
FIGURE 14



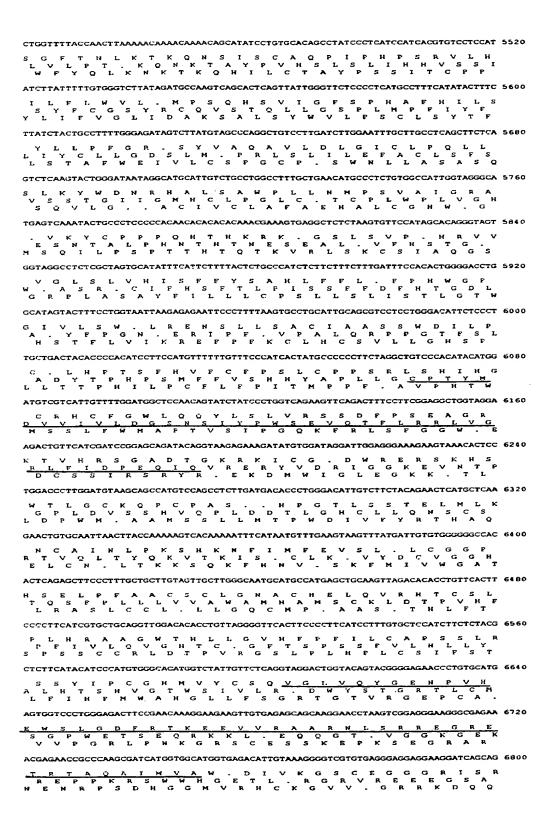


CAGGTGAGGGAAGCAAACTTGGTTTCTGCTGGGAATGGAAGTTATGTGGATTGTTTATAATTGGGACCATTATGGCTAAA	2800
R. GKQTWFLLGMEVMWIVYNWDHYG. LGEGSKLGFCWEWKLCGLFIIGTIMAK QVREANLVSAGNGSYVDCL.LGPLWLK	2880
ATCTYGCGGGCGCTCAGGTCGGAGGTTAATACCGATGCTATATTTCCTGTGTGCACTCATGTTCTTAGACACCCAAATGG	2000
V L A G A Q V G G . Y R C Y I S C V H S C S . T P K W I ? R A L R S E V N T D A I F P V C T H V L R H P N G S ? G R S G R R L I P M L Y F L C A L M F L D T Q M	
CAGTGGCCAAAACTTCCTCTGGCTTGTACCTCATTATCTAAACCTTTGTACCTAATTATCTAAAACCTTGGTCCTAAACT	2960
Q W P K L P L A C T S L S K P L Y L I I . N L G F K L S G Q N F L W L V P H Y L N L C T . L S K T L V L N A V A K T S S G L Y L I I . T F V P N Y L K P W S . T	
CACAGACATGAGGCACAGAAAAGAGACGTGTCTCTCATCTTCCATTCGGTTACACTGATTCCTACCTTCCCTGCTTCT	3040
H R H E G T E K R R V S H L P F G Y T D S Y L P C F S T D M R A Q K R D V S L I F H S V T L I P T F P A S F Q T . G H R K E T C L S S S I R L H . F L P S L L L	
CCCTGCCATTGGTGCTCCTTGGTGCCTGAGGCATAATTGCCTTACTATTGTGGTCAGAACTCTGGGTTCGCCTAACGACCG	3120
5 L P L V L L G A . G T I A L L C G Q N S G F A . R P P C H W C S L V P S A . L P Y Y V V R T L G S P N D R P A I G A P W C L R H N C L T M W S E L W V R L T T	
agctacagtttctggtctcatagccctgccaatttcctggattaaaaaaaa	3200
SYSFWSHSPANFLD.KKAHI.NTFSE ATVSGLIALPISWIKKKRLTYKIPFL ELOFLVS.PCQFPGLKKKGSHIKYLF.	
aaatgagcacagtgtgagttgaagttagattttgggggatggaggttgcttggatgcaaagacaagacagtagacaag	3280
NEHSVS.S.ILGDGGLLGCKEQDSRE KMSTV.VEVRFWGMEGCLDAKSKTVEK K.AQCELKLDFGGWRVAWMQRARQ.RR	
AGANTCATGGGAGGGATAAGAGGCTGGANTTTTTCCCTGCTAGTGCCCTNTANTCTTTGTTTCCTAAANTAACAGCTCTG	3360
ENHGRDKRLEFFPASAL.SLFPKITAL RIMGGIRGWNFSLLVPYNLCFLK.QL. ESWEG.EAGIFPC.CPIIFVS.NNSS	
attttatoggaattooggteaggaaaggaateagtaggeaeagatgggaeeeeeaggeetaaagtttgaggaaa	3440
I LWELGSGERNQ. AQMGPQAWTKV.GN FYGNWGQEKGISRHRWDPKRGLKFEE DFMGIGVRRKESVGTDGTPSVD. SLRK	
ctatoggagtaggcaaggogtgtttgtaaggtggatgagatga	3520
Y G S R Q G V F V R W M R . G D C G G G E S W G . I M G V G K G C L . G G . D E E I V V G G S L G G D R L W E . A R G V C K V D E M R R L W W G G V L G V I G	2600
ACCCTTAACAGGGATAGATGGCAAACTGTGTGTGGGCAGGCCGGTGGTTCCACCCAC	3600
DP.QG.MANCVWAGRWFHPLN.R.GWQ TLNRDRWQTVCGQAGGSTHLISVEVGR PLTGIDGKLCVGRPVVPT.LALRLA	2422
gctggaaggagccagcactctcaaccttggagaaagtgcaagtgtgacaagaagaaacaacagaaaaaaaa	3680
G W K E P A L S T L E K V Q V . Q E E T E R G D T R A A G R S Q H S O P W R K C K C D K K K Q K E E T P G G L E G A S T L N L G E S A S V T R R N R K R R H P G AGGGAGCTCCTTGCCATGGTTTCCCATGGCCTTGGGTTTGGGAAAGAATTAGGAAAGGGTGGTGACTCTGCATCCTCA	3760
	•
G S S L P S F L P M A L A L G R I R K G W . L C I L Q G A P C H R F F P W P W L W E E L G K G G D S A S S R E L L A I V S S H G P G F G K N . E R V V T L H P Q	3840
GAAAAGCCUTCTCTCCCTCTTTGGACTCTCGAGGCTTAGAGAGGAGAATGTGTAGGAGGAATGATGTGGAAAGAGTAACT	
R K A L S P S L D S R G L E R R M C R R N D V E R V T E K P S L P L W T L E A . R G E C V G G M M W K E . L K S P L S L F G L S R L R E E N V . B E . C G K S N	2020
tgacctatccagatgtgtgtgtgaatgagatttcaggaatgagaatggaaatacggctgtgtgttcagcatggccgagggc	3323
. PIQMCL. MRFQE. EWKYSCASAWPRA DLSRCVCE. DFRNENGNTAVLQHGRG LTYPDVSVNEISGMRMBIQLCFS MAEG	4000
CTTAGGAT CCCTCACCCCCACACGCACAGGAAGAGAATCATCCAATCATCCCACCTGGGGTTCTGAGGACATGACATTGAC	-000
LGSLTPTPQEENHPIIPPGVLRT.H. P. DPSPPPHRKRIIQSSHLGF.GHDID LRIPHPHPTGRESSNHPTWGSEDMTLT	4000
ACAGAGCAGGAGAGCTGAGATAGAAACACTCCCTCCTGTCTTGTCTCCCACTAAGCCTCACCAGTCCTTCATTAACTGAT	4080
H RAGELR. KHSLLSCLPLSLTSPSLTD TEQES. DRNTPSCLVSH. ASPVLH. LI	

4:



٠:



GGAGAGGGAGAGGGTCTGGAGTGTAGTGTATACATCACAAGATGCTCTGGGCGCTTATCTTTATCTGCATGCCAGAAGTT 6880	
ERERVWSVYTSQDALGAYLYLHARS GRGRGSGV_CIHHKMLWALIFICMPEV GEGEGLECSVYITRCSGRLSLSACQKF	
CGTGGAGGAAGGCTAGGTTGCTGTCACCATACTCTCTTACTGTATTTGCATTTTATGGTGTCTGTGGGTGTATCTCTC 6960	
S W R K A R L L S P Y S L L L Y L H F M V S V G V S L R G G R L G C C H H T L S Y C I C I L W C L W V Y L S V E E G . V A V T I L S L T V F A F Y G V C G C I S	
CTTGTCTGTTCTGTTTCTGCACACAGAACTCCATCTTTCCTCTTCTACTCCTGCGTCAATTCTGATACCTAGCTTCTCAA 7040	
L V C S V S A H R T P S F L F Y S C V N S D T . L L N L S V L F L H T E L H L S S S T P A S I L I P S F S P C L F C F C T Q N S I F P L L L R Q F . Y L A S Q	
CCACTCACGCCCTAGTATTCTTTTCAAACATGACTCTAAACCTCTGGGGAGGCTACATGACCTGACTGTCTTTATTCTCC 7120	
H S R P S I L F K H D S K P L G R L H D L T V F I L T T H A L V F F S N M T L N L W G G Y M T . L S L F S P L T P . Y S F Q T . L . T S G E A T . P D C L Y S P	
AGTICCTIGATCTIGICAACCCAAGTGTITGCTGAATGAATCTATAAATAAATAATGCTTGTACATATTTACACTGATGA 7200	
Q F L D L V N P S V C . M N L . I N N A C T Y L H S S L I L S T Q V F A E . I Y K . I M L V H I Y T D D V P . S C Q P K C L L N E S I N K . C L Y I F T L M	
CAGATTATTTTATATGTTCCGTGCCATCTAAACAGTCAAGTTGTGACTCTGTGCCAGTTTGCATGCTAGATACTGTTGGG 7280	
Q I I L Y V P C H L N S Q V V T L C Q F A C . I L L G R L F Y M F R A I . T V K L . L C A S L H A R Y C W T D Y F I C S V P S K Q S S C D S V P V C M L D T V G	
GAATGGTGTAGAAGACATCTGACCTCAGTGAACTGCTGACAGTGTTAATACACTATACGGGCATGCCTGCATGCA	
NGVEDI. PQ.TADSVNTLYGHACMQA GMV. KTSDLSELLTVLIHYTGMPACKP EWCRRLISVNC. QC.YTIRACLHASL	
GTGTGTATGTGCATGCATATGCACACACATACATATGACCATATAGCATTCTTTTATCTCTCTTTAGCACAGAAGGGT 7440	
C V Y V H A Y A H T Y I . P Y S I L L S L F L A Q K G V C M C M H M H T H T Y D H I A F F Y L S S . H R R V C V C A C I C T H I H M T I . H S F I S L L S <u>T E G</u>	
TCAGTCAGTCCCGGGGGGGACGACCAGAGGCCGCTAGGCTGCTGGTAGTTGTCACTGATGGAGAGTCCCATGATGGAGAG 7520	
S V S P G G D D Q R P L G C W . L S L M E S P M M E R Q S V P G G T T R G R . A A G S C H . W R V P . W R E S Q S R G G R P E A A R L L V V V T D G E S H D G E	
GAACTTCCAGCAGCGCTAAAGGCCTGTGAGGCTGGCAGAGTGACACGTTATGGGATTGCGGTGAGACTTGATCAAGTCCA 7600	
N F Q Q R . R P V R L A E . H V M G L R . D L I K S G T S S S A K G L . G W Q S D T L W D C G E T . S S P E L P A A L K A C E A G R V T R Y G I A V R L D Q V Q	
GT1GTTTTGTTTTGTGTGTATCGTGTGTGTGTGTGTGTGTGTG	
S C F V L C C I V C V C V C V C V C V C V Y V . Y V V L F C V V S C V C V C V C V C V C V C M C D M L F C F V L Y R V C V C V C V C V C V C V C V I	
GTGTGCATGCATCAGTGCACATACCATAGTGTGTATATGCGGGTCAGAGAACCACCTCAGATGTTGGTCCTCACCTTCCA 7760	
V C M H Q C T Y H S V Y M R V R E Q P Q M L V L T F H C A C I S A H T I V C I C G S E N N L R C W S S P S C V H A S V H I F . C V Y A G Q R T T S D V G P H L P	
TCTTGTTCCAAACTGGATATCTTGTTCACTTCGGCATACAATAAGCCAGATTAGCTGACCCACAAGTCTTGGGCAGGTCT 7840	
L V P N W I S C S L R H T I S Q I S . P T S L G Q V I L F Q T G Y L V H F G I Q . A R L A D P Q V L G R S S C S K L D I L F T S A Y N K P D . L T H K S W A G L	
TCTGTCTCAGCCTCCTGTCTCTTGGTTTGAGGCATTCTGGAATTTACAGATAAGCTTGATATCGAATTCCTGCAGCCCGG 7920	
FCLSLLSLGLRHSGIYR.A.YRIPAAR SVSASCLLV.GILEFTDKLDIEFLQPG LSQPPVSWFEAFWNLQISLISNSCSP	
GGGATCCACTAGTTCTAGAGCGGCCGCCACCAAGGGAG 7958	
G I H . F . S G R H Q G S G S T S S R A A T K G	

FIGURE 15f

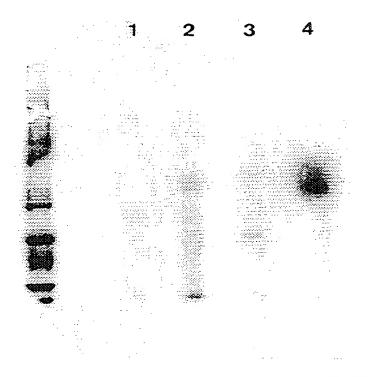


FIGURE 16

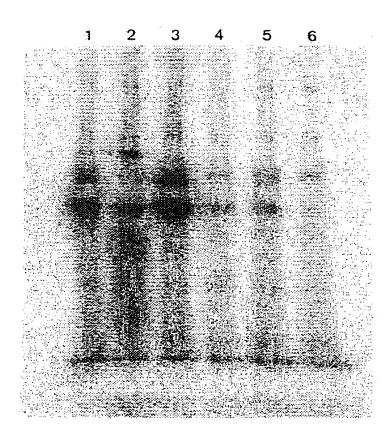


FIGURE 17